

1

SEQUENCE LISTING

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<120> Novel genes and their use in the modulation of obesity, diabetes and energy imbalance

<130> 2309315/TDO

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<150> 60/141441

<151> 1999-06-29

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 1669

<212> DNA

<213> mammalian

<220>

52213 CDS

-333- (43) - (1107)

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Gly Ile Phe Leu Cys Leu Ile Phe Leu Glu Lys Ser Trp Gly Gln Ile

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caa atg tcg tgt tgg ccc aag cct ttg att cca gaa ctt gag agg cag 150
Gln Met Ser Cys Trp Pro Lys Pro Leu Ile Pro Glu Leu Glu Arg Gln
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aga tgc acc gtt gta aca cca aaa gtc ttc cga gtc gga gaa tat gaa 198
Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val Gly Glu Tyr Glu
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Gln Val Thr Phe Glu Ala His Gly His Thr Asp Pro Phe Asp Val Thr
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tct gta cat tta tca cca gaa aat aaa ttc aaa aac tct aca atc tta Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn Ser Thr Ile Leu	342
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aca att cag ccc aaa cag ttg tct gaa ggg caa aac tcg tct tcg cat Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn Ser Ser His	390
105 110 115	
gtg tat ttg gaa gtt gtg tcc aag cat ttt tca aca tca aaa ata atg Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Thr Ser Lys Ile Met	438
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tca atc gtc tat gac aat ggc act ctc ttc att cag act gac aag cct Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln Thr Asp Lys Pro	486
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atc acc tct ttc cct gac ttc agg att cct act aac cct aag ccc ggt Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn Pro Lys Pro Gly	678
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ctc gtt cca aca agt gat ctg gaa cac cca atg gaa gaa gca cgt ggc Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu Glu Ala Arg Gly	822
245 250 255 260	
ctg agt ctc cag cca aaa aag tcc ctg caa gag atg ata cat gag cca Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met Ile His Glu Gln	870
265 270 275	
gct tcg aaa tac aaa cat cca gta ctg aag aaa tgt tgt tat gat gga	918

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Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys Cys Tyr Asp Gly
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Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg Val Ala Arg Val
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aaa ata ggc cca aac tgt gtc aga gcc ttc agt gaa tgc tgt gcc ctg 1014
Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu Cys Cys Ala Leu
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Ala Ser Glu Asn Thr Phe Lys Asn Ile Leu Met Ser Arg Pro Asp Asp
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Leu Glu Arg Gln Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val

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45

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Phe Asp Val Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Asn Ala Asn
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Tyr Ser Ser Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn
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Ser Thr Ile Leu Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn
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Ser Ser Ser His Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Thr
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Ser Lys Ile Met Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln
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Thr Asp Lys Pro Val Tyr Thr Pro Glu Gln Pro Val Lys Val Ala Val
 145 150 155 160

Tyr Ser Leu Asp Glu Ala Leu Lys Pro Val Thr Arg Glu Thr Val Leu
 165 170 175

Thr Phe Ile Asp Pro Glu Gly Ser Glu Val Gly Ile Val Glu Gly Ser
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Asn His Thr Gly Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn
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Pro Lys Pro Gly Arg Trp Met Ile Lys Ala Lys Tyr Arg Glu Asp Ala
 210 215 220

Ser Thr Ala Gly Thr Thr His Phe Glu Ile Lys Glu His Asp Lys Ala
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Phe Lys Ile Ala Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu
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Glu Ala Arg Gly Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met
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Ile His Glu Gln Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys
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Cys Tyr Asp Gly Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg
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Val Ala Arg Val Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu
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<222> (20)..(589)

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ccg	gcg	ctg	gag	acc	gag	ggc	ctg	agg	ttc	ctg	cac	gtc	aca	gtg	ggc	100
Pro	Ala	Leu	Glu	Thr	Glu	Gly	Leu	Arg	Phe	Leu	His	Val	Thr	Val	Gly	
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tcc	ctg	ctg	gcc	agc	tat	ggc	tgg	tac	gtc	ctc	ttc	agc	tgc	atc	ctt	148
Ser	Leu	Ala	Ser	Tyr	Gly	Trp	Tyr	Val	Leu	Phe	Ser	Cys	Ile	Leu		
		30			35			40								

ctc	tac	att	gtc	atc	cag	aag	ctc	gtc	cga	ttg	agg	gtt	ttg	agg		196
Leu	Tyr	Ile	Val	Ile	Gln	Lys	Leu	Ser	Val	Arg	Leu	Arg	Val	Leu	Arg	
		45			50			55								

cag	agg	cag	ctg	gac	cag	gct	gac	gct	gtt	ctg	gaa	cct	gat	gct	gtt	244
Gln	Arg	Gln	Leu	Asp	Gln	Ala	Asp	Ala	Val	Leu	Glu	Pro	Asp	Ala	Val	
		60			65			70			75					

gtt	aag	cga	caa	gag	gct	tta	gcc	gct	gct	cgt	ttg	aga	atg	cag	gaa	292
Val	Lys	Arg	Gln	Glu	Ala	Leu	Ala	Ala	Ala	Arg	Leu	Arg	Met	Gln	Glu	
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gaa gaa gaa aaa agg aga cag aag att gaa atg tgg gac agc atg caa	388		
Glu Glu Glu Lys Arg Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln			
110	115	120	
gaa ggc aga agt tac aga aga aat cca gga agg cct cag gaa gaa gat	436		
Glu Gly Arg Ser Tyr Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp			
125	130	135	
ggt cct gga cct tct act tca tca tct gtc acc cgc aaa gga aaa tct	484		
Gly Pro Gly Pro Ser Thr Ser Ser Val Thr Arg Lys Gly Lys Ser			
140	145	150	155
gac aaa aag cct ttg agg gga aat ggt tat aac cct ctg acg ggt gaa	532		
Asp Lys Lys Pro Leu Arg Gly Asn Gly Tyr Asn Pro Leu Thr Gly Glu			
160	165	170	
ggg ggt gga acc tgc gcc tgg aga cct gga cgc agg ggc cca tca tct	580		
Gly Gly Gly Cys Ala Trp Arg Pro Gly Arg Arg Gly Pro Ser Ser			
175	180	185	
ggt gga tga agctaagacc cttgttagtg tcgctttgac attagcaagg.	629		
Gly Gly			
190			
tgaaccctta accctcaact cagttgcattt acgcacactt tcacagtgac tagccaagg	689		
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35 40 45

Gln Lys Leu Ser Val Arg Leu Arg Val Leu Arg Gln Arg Gln Leu Asp
50 55 60

Gln Ala Asp Ala Val Leu Glu Pro Asp Ala Val Val Lys Arg Gln Glu
65 70 75 80

Ala Leu Ala Ala Ala Arg Leu Arg Met Gln Glu Asp Leu Asn Ala Gln
85 90 95

Val Glu Lys His Lys Glu Lys Leu Arg Gln Leu Glu Glu Glu Lys Arg
100 105 110

Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Arg Ser Tyr
115 120 125

Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp Gly Pro Gly Pro Ser
130 135 140

Thr Ser Ser Ser Val Thr Arg Lys Gly Lys Ser Asp Lys Lys Pro Leu
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Ala Trp Arg Pro Gly Arg Arg Gly Pro Ser Ser Gly Gly
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<220>
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 <222> (31)..(594)

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 Ser Ala Arg Pro Ala Leu Glu Thr Glu Gly Leu Arg Phe Leu His Thr
 10 15 20

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 Thr Val Gly Ser Leu Leu Ala Thr Tyr Gly Trp Tyr Ile Val Phe Ser
 25 30 35 40

tgc atc ctt ctc tac gtg gtc ttt cag aag ctt tcc gcc cgg cta aga 198
 Cys Ile Leu Leu Tyr Val Val Phe Gln Lys Leu Ser Ala Arg Leu Arg
 45 50 55

gcc ttg agg cag agg cag ctg gac cga gct gcg gct gct gtg gaa cct 246
 Ala Leu Arg Gln Arg Gln Leu Asp Arg Ala Ala Ala Val Glu Pro
 60 65 70

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 Asp Val Val Val Lys Arg Gln Glu Ala Ala Ala Ala Arg Leu Lys
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atg caa gaa gaa cta aat gcg caa gtt gaa aag cat aag gaa aaa ctg 342
 Met Gln Glu Glu Leu Asn Ala Gln Val Glu Lys Glu Lys Leu
 90 95 100

aaa caa ctt gaa gaa gaa aaa agg aga cag aag att gaa atg tgg gac 390
 Lys Gln Leu Glu Glu Lys Arg Arg Gln Lys Ile Glu Met Trp Asp
 105 110 115 120

agc atg caa gaa gga aaa agt tac aaa gga aat gca aag aag ccc cag 438
 Ser Met Gln Glu Gly Lys Ser Tyr Lys Gly Asn Ala Lys Lys Pro Gln
 125 130 135

gag gaa gac agt cct ggg cct tcc act tca tct gtc ctg aaa cgg aaa 486
 Glu Glu Asp Ser Pro Gly Pro Ser Thr Ser Ser Val Leu Lys Arg Lys
 140 145 150

tcg gac aga aag cct ttg cgg gga gga ggt tat aac ccg ttg tct ggt 534
 Ser Asp Arg Lys Pro Leu Arg Gly Gly Tyr Asn Pro Leu Ser Gly
 155 160 165

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Glu Gly Gly Gly Ala Cys Ser Trp Arg Pro Gly Arg Arg Gly Pro Ser			
170	175	180	
180			

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Ser Gly Gly	
185	

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30			

Tyr Gly Trp Tyr Ile Val Phe Ser Cys Ile Leu Leu Tyr Val Val Phe			
35	40	45	
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Gln Lys Leu Ser Ala Arg Leu Arg Ala Leu Arg Gln Arg Gln Leu Asp			
50	55	60	
60			

Arg Ala Ala Ala Ala Val Glu Pro Asp Val Val Val Lys Arg Gln Glu			
65	70	75	80
75	80		

Ala Leu Ala Ala Ala Arg Leu Lys Met Gln Glu Glu Leu Asn Ala Gln			
85	90	95	
95			

Val Glu Lys His Lys Glu Lys Leu Lys Gln Leu Glu Glu Lys Arg	
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300

105

110

Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Lys Ser Tyr
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11

120

125

Lys Gly Asn Ala Lys Lys Pro Gln Glu Glu Asp Ser Pro Gly Pro Ser
130 135 140

130

135

140

Thr Ser Ser Val Leu Lys Arg Lys Ser Asp Arg Lys Pro Leu Arg Gly
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Arg Pro Gly Arg Arg Gly Pro Ser Ser Gly Gly
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Leu Ser Pro His Ser Val Ala Ser Met Leu Ser Ala Val Glu Ala Gly
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Thr Val Phe Leu Leu Val Thr Ser Leu Pro His
          20          25

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Thr Arg

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